

Fri Mar 22 08:49:00 2002

pct-us01-24104a-1.rge

Page 1

GenCore version 4.5
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OM nucleic - nucleic search, using sw model
Run on: March 20, 2002, 17:19:05 : Search time 4182.4 Seconds
(without alignments)
10145.071 Million cell updates/sec

Title: PCT-US01-24104a-1
Sequence: 1 tctgattccaccctccagca.....tataataaagatataag 2572

Scoring table: IDENTITY: 100, GAP: 10, GAPEXT: 1.0

Searched: 1472140 seqs, 8248589755 residues

Total number of hits satisfying chosen parameters: 2944280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: GenBank

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2: gb_hg:.*
3: gb_in:.*
4: gb_ov:.*
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34: gb_ov:.*
35: gb_ov:.*
36: gb_ov:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2572	100.0	2572	D88213	D88213 Homo sapien
2	2469.8	96.0	2653	AF081163	AF081163 Homo sapi
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4	1609	62.6	189149	AC046171	AC046171 Homo sapi
5	1609	62.6	190100	AC016889	AC016889 Homo sapi
6	1609	62.6	204685	AC035866	AC035866 Homo sapi
7	1144.8	44.5	200828	AC025424	AC025424 Homo sapi
8	1144.8	44.5	250437	AL590969	AL590969 Mus muscu
9	1017.8	39.6	2501	AF067406	AF067406 Homo sapi
10	1017.8	39.6	1040	AF067406	AF067406 Homo sapi
11	990.6	38.5	1624	AB019242	AB019242 Bos tauru
12	954.6	37.1	2664	BOVFERA	BOVFERA Bos tauru
13	954.6	37.1	2664	BOVFERA	BOVFERA Bos tauru
14	953	37.1	2605	AF015774	AF015774 Bos tauru
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16	781	30.4	2614	AF054831	AF054831 Mus muscu
17	746.2	29.0	2073	AF047485	AF047485 Homo sapi
18	742.2	28.9	14357	AF078705	AF078705 Mus muscu
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20	627.4	24.4	1051	AF078705	AF078705 Mus muscu
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23	245.8	9.6	2375	AF078705	AF078705 Mus muscu
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28	202.4	7.9	9903	AF078705	AF078705 Mus muscu
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42	58.2	2.3	1156	AF078705	AF078705 Mus muscu
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ALIGNMENTS

RESULT 1
LOCUS D88213 2572 bp mRNA
DEFINITION Homo sapiens mRNA for retine-specific amine oxidase, complete cds.
ACCESSION D88213.1 GI:1906805
VERSION D88213.1
KEYWORDS RAO: AOC2; Retina-specific amine oxidase.
SOURCE Homo sapiens etna cDNA to mRNA, clone_11b: human retina 5'-stretch
CDNA library (clontech).
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 2572)
Shimizu, N.
Direct Submission
Submitted (02-OCT-1996) to the DDBJ/EMBL/GenBank databases.
Nobuyoshi Shimizu, Kato University School of Medicine, Department
of Molecular Biology, 35 Shinanomachi, Shinjuku-ku, Tokyo 160-8582,
Japan (E-mail: shimizu@med.kato.ac.jp).
Tel: 81-3-3351-2370 (ex. 2720), Fax: 81-3-3351-2370)

REFERENCE
AUTHORS
TITLE
JOURNAL

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/product-retina-specific amine oxidase
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Matches 2572;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

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pct-us01-24104a-1.rge

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DEFINITION	AF081363	2653 bp	mrna	PRI	17-JUN-1999
LOCUS					
REFERENCE	Homo sapiens retina copper-containing monamine oxidase (AOC2)				
ACCESSION	AF081363				
VERSION	AF081363.1	GI:5081318			
KEYWORDS					
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Placentalia; Catarrhini; Hominoidea; Homo.				
AUTHORS	1 (bases 1 to 2653)				
TITLE	Zhang, X. and McIntire, W. S.				
JOURNAL	Human Copper-Containing Amine Oxidases				
REFERENCE	2 (bases 1 to 2653)				
AUTHORS	Zhang, X. and McIntire, W. S.				
TITLE	Direct Submission				
JOURNAL	Submitted (23-JUL-1999) Molecular Biology (151-S), VA Medical Center, 4150 Clement Street, San Francisco, CA 94121, USA				
COMMENT	This is the gene for a long form of the human retina (RAO-n). Cloning and sequencing of a truncated form of this gene has been published: Imanura et al. Genomics 40:277-283 (1997).				
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Raye

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FEATURE			
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DEFINITION	M.musculus gene for tyrosine kinase receptor.		
ACCESSION	X59560		04-MAR-1994
VERSION	X59560.1		
KEYWORDS	tyrosine kinase receptor.		
SOURCE	house mouse.		
ORGANISM	Mus musculus		
	Eukaryota; Mammalia; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclurognathia; Muridae; Murinae; Mus.		
REFERENCE			
AUTHORS	Mansukhani, A.		
TITLE	Direct Submission		
JOURNAL	Submitted (22-MAY-1991) to Mansukhani, New York School of Medicine, Dept of Microbiology, 550 First Avenue, New York NY 10016, USA		
REMARK			
REFERENCE			
AUTHORS	Rescigno, J., Mansukhani, A. and Basalico, C.		
TITLE	A putative receptor tyrosine kinase with unique structural topology		
JOURNAL	Oncogene 6 (10), 1909-1913 (1991)		
MEDLINE	82019811		
REFERENCE	3 (bases 1 to 4126)		
AUTHORS	Mansukhani, A.		
TITLE	Direct Submission		
JOURNAL	Submitted (03-MAR-1994) to Mansukhani, New York School of Medicine, Dept of Microbiology, 550 First Avenue, New York NY 10016, USA		

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: March 20, 2002, 20:18:27 ; Search time 4182.4 seconds

(without alignments)
12728.672 Million cell updates/sec

Title: PCT-US01-24104A-2

Perfect score: 3227
Sequence: 1 gctcggaacagccgctgca.....aaaaaaaaaaaaaaaaaa 3227

Scoring table:

IDENTITY NUC
Gapop 10.0, Gapeat 1.0

Searched: 1472140 seqs, 8248589755 residues

Total number of hits satisfying chosen parameters: 2944280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

- 1: GenBank:*
- 2: gb_ba:*
- 3: gb_hlg:*
- 4: gb_in:*
- 5: gb_om:*
- 6: gb_ov:*
- 7: gb_pac:*
- 8: gb_ph:*
- 9: gb_pl:*
- 10: gb_pr:*
- 11: gb_ro:*
- 12: gb_sts:*
- 13: gb_sy:*
- 14: gb_un:*
- 15: gb_vl:*
- 16: em_ba:*
- 17: em_fun:*
- 18: em_hum:*
- 19: em_in:*
- 20: em_om:*
- 21: em_or:*
- 22: em_ov:*
- 23: em_pac:*
- 24: em_ph:*
- 25: em_pl:*
- 26: em_ro:*
- 27: em_sts:*
- 28: em_sy:*
- 29: em_un:*
- 30: em_vl:*
- 31: em_hgo_hum:*
- 32: em_hgo_lav:*
- 33: em_hgo_rod:*
- 34: em_hlg_hum:*
- 35: em_hlg_lav:*
- 36: em_hlg_rod:*
- 37: em_hlg_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3227	100.0	3227	9	HUMTYRKINR
2	3217.4	99.7	3227	6	MT6125
3	3178.8	98.5	3254	6	115526
4	3037.6	94.1	3116	9	115525
5	3037.6	94.1	3116	9	HSUP025
6	2060	63.8	4126	10	551125
7	2058	63.8	4072	10	MT6125
8	740.4	22.9	129402	9	AC011310
9	516.2	16.0	2550	6	AC011310
10	516.2	16.0	2742	6	AJ39860
11	516.2	16.0	3611	6	AR094422
12	516.2	16.0	3611	6	AR094459
13	516.2	16.0	3611	6	AR103003
14	516.2	16.0	3611	6	AR105287
15	516.2	16.0	3611	6	AR105287
16	516.2	16.0	3611	6	HS005682
17	516.2	16.0	3949	9	HUMSKY
18	516.2	16.0	4364	6	AJ39859
19	509.8	15.8	2779	9	HSU18934
20	508.8	15.8	3307	6	AR042418
21	508.8	15.8	3307	6	AR042418
22	508.8	15.8	3307	6	AR054633
23	506.4	15.7	3276	10	RATSKY
24	506.4	15.7	2530	6	AJ39858
25	506.4	15.7	3845	10	AB000828
26	506.4	15.7	3309	10	MMTYR03
27	506.4	15.7	3785	6	AR094163
28	506.4	15.7	3785	6	AR103007
29	506.4	15.7	3785	6	AR105291
30	506.4	15.7	3785	6	IR0848
31	506.4	15.7	3785	10	MMU05683
32	506.4	15.7	3907	10	MMU18342
33	506.4	15.7	3919	6	AJ39857
34	506.4	15.7	3919	10	MMU18933
35	489.6	15.2	3037	5	CHICKEN
36	482	14.9	3024	10	AF208235
37	477.8	14.8	4961	5	GDUT0045
38	461.8	14.5	4418	10	AREVRYK
39	459.2	14.0	3010	14	AREVRYK
40	451.2	14.0	3564	10	MMU21301
41	450	13.9	3031	9	HSU02566
42	439.6	13.6	3608	9	HSU08023
43	439.6	13.6	3635	6	IJ2202
44	439.2	13.6	1951	10	MUSRPRKA
45	399.2	12.4	2779	6	ELI2132

ALIGNMENTS

RESULT	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	TITLE	JOURNAL	MEDLINE	REFERENCE	AUTHORS
1	HUMTYRKINR	Human tyrosine kinase receptor (axl) mRNA, complete cds.	MT6125.1	GI:292869	tyrosine kinase receptor.	Homo sapiens	CDNA to mRNA.	14-JAN-1995					
2	HUMTYRKINR	Human tyrosine kinase receptor (axl) mRNA, complete cds.	MT6125.1	GI:292869	tyrosine kinase receptor.	Homo sapiens	CDNA to mRNA.	14-JAN-1995					
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Oy	2581	acggaatccctcctatgcatacatgagtcggagggtcggaagtattaccgaaaccttgcgagctg	2640
Db	2581	ACGGAATCCCTCCTCATGTGCMAATCGATGATGGAGGTGAGACTTATCTGAAACCCCTGAGACTG	2640
Oy	2641	caggagaagctgagaccgcccaaacacagccagagaccctaagaattctcttgagctctcacg	2700
Db	2641	CAGGAGAAGCTGAGACCCTACCCCCAACCCAGCACGCCCTTAAGATTCTCTTAGCTGCCCTCACTG	2700
Oy	2701	cgagctgaggctccactctgctggagagcttatctctctgcccctccacaaccttagccccg	2760
Db	2701	CGAGCTGAGGCTCCACTCTGCTGGAGAGCTTGCTGAGCCCTTAGCTCTCTGCCCTTCACACACCCCTACCCC	2760
Oy	2761	ctcagagctctgtaataaggagctccccaagagccccaagggcagaagatggcgctgagaca	2820
Db	2761	CTCAGAGCTCTGTATATAGAGGCTCTCCACAGCAGCCCCAAGGCGAGAGATGGTGGCTTGAGACA	2820
Oy	2821	accctccacctgggaactccctccctcaagatcccaagctaaagctctgacactcgagaaaactc	2880
Db	2821	ACCTCCACCTGGGACTCTCCCTCTCAGATCCAAGCTAAGCACTCCACATGGGGAANAATC	2880
Oy	2881	caacctccgaactttccacaccaagcactatacccaactctgaagccctgctctctctactca	2940
Db	2881	CACCTCCGACCTTTCCACCCACGACCCCTTATCCCACTTGACGACCTGTCTCTCTACTCA	2940
Oy	2941	tccacactlccatcccaagaagagctcccccctctctctctgagctagacatacactgaag	3000
Db	2941	TCCACACTCCATCCACAGAGAGGTCCCTCCCTCTCTCTGTGCATACATCACTTGAAAG	3000
Oy	3001	cagtagcatacccatcctgcaaaaaagaagggttgtatgtcaataatcgaaagccctccag	3060
Db	3001	CAGTAGCATACCATCTCTGTAAAAAGAGGGGTGTGATGTCAATATCTGAACCCCTCCAG	3060
Oy	3061	ggtctaatatcccaagaagctctaaagatcaaaggtcttaaagagctcgaattcaaaagttcta	3120
Db	3061	GGTCTAATATCCAGACACTCTAAGCTCCAAAGGTTTAAAGAGCTTAATTTCAAAGTTCTA	3120
Oy	3121	ggcttcaaaagctctgtgagctcttggtctcctcaagagctgaaatccaaatcgaagctccta	3180
Db	3121	GGTTTCAAAAGCTGTAGAGCTTGTGTTCTTAAGACCTCAAAATTTCCAATCTCTAATT	3180
Oy	3181	ctattaagagggcctaaaggtctctaaagcnaaaaaaaaaaaaaaaaaa 3227	
Db	3181	CTATTAAAGTCTTAAGCTTTAAGCAAAAAAAAAAAAAAAAAAAAAA 3227	
RESULT	2		
LOCUS	115526	3227 bp	DNA
DEFINITION	Sequence 3 from patent US 5468634.	PAT	02-APR-1996
ACCESSION	U115526		
VERSION	U115526.1	GI:1250434	
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	Unclassified.		
AUTHORS	1 (bases 1 to 3227)		
TITLE	Liu,E.T.		
JOURNAL	Axi Oncogene		
FEATURES	Location: US 5468634-A § 21-NOV-1995;		
source	1..3227		
	Location:Qualifiers		
	1..3227		
BASE COUNT	700 a	971 c	938 g
ORIGIN	700 a	971 c	938 g
	626 t		
Query Match	99.7%	Score 3217.47	DB 6; Length 3227;
Best Local Similarity	99.8%	Pred. No. 0;	
Matches 3221;	Conservative 0;	Mismatches 6;	Indels 0; Gaps 0
Oy	1	gctgggcaaaagccggtgcaagagctccctctgcccctgtgcacaggaaggcagtcgcaaa	60
Db	1	GCTGGGCAAGCGCGGTGCAAGGCTCCCTCTGCCCCTGTGCCAGGACGACATGCTCCAAA	60